In the Claims:

Please amend the Claims as follows.

12. (Amended) A method for generating a secondary library of scaffold protein sequences comprising:

a) receiving a library of primary sequences generated utilizing a force field calculation;

b) generating a probability distribution table of amino acid residues in a plurality of variant positions from said primary sequences; and

c) combining a plurality of said amino acid residues to generate a secondary library of secondary sequences; wherein at least one of said secondary sequences is different from said primary sequences.

13. (Amended) A method according to claim 12, wherein said force field calculation is Self-Consistent Mean Field (SCMF).

15. (Amended) A method according to claim 14, wherein a Protein Design Automation program is used to recombine said secondary library.

16. (Amended) A method for generating a secondary library of scaffold protein variants comprising:

a) receiving a library of primary sequences generated utilizing an alignment program;

b) generating a probability distribution table of amino acid residues in a plurality of variant positions from said primary sequences;

c) combining a plurality of said amino acid residues to generate a secondary library of secondary sequences, wherein at least one of said secondary sequences is different from said primary sequences; and

d) computationally ranking said secondary library.

18. (Amended) A method according to claim 17, wherein a Protein Design Automation program is used to recombine said secondary library.

24. (Amended) A method according to claim 22 wherein said pooled oligonucleotides are added in amounts that correspond to the frequency of the mutation.

Please add the following new claims:

26. (New) A method for generating a secondary library of scaffold protein sequences comprising:

a) generating a probability distribution table of amino acid residues in a plurality of variant positions from a force field calculation; and